

Sequence Search Summary

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2003, 05:40:34 ; Search time 6430 Seconds
(without alignments)
8461.867 Million cell updates/sec

Title: US-09-935-757-1
Perfect score: 1330
Sequence: 1 accagtggagccggttgccat.....tcacctttcagcagacgccg 1330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1330	100.0	1330	6	AX394669	Applicants Sequence
	2	1330	100.0	2086	6	AX394673	AX394673 Sequence
	3	1330	100.0	333150	1	AP005277	Nakagawa GenBank Corynebact
	4	1330	100.0	349980	6	AX127146	CP1108790 Sequence
	5	639	48.0	639	6	AX121325	AX121325 Sequence
	6	639	48.0	639	6	BD163442	BD163442 Novel pol
	7	514	38.6	300750	1	AP005217	AP005217 Corynebact
	8	267.6	20.1	1520	1	MSU87307	U87307 Mycobacteri
	9	251	18.9	1810	1	MAU87308	U87308 Mycobacteri
	10	247.8	18.6	771	6	AX452170	AX452170 Sequence
	11	247.8	18.6	771	6	AX663940	AX663940 Sequence
	12	247.8	18.6	3690	1	MTU87242	U87242 Mycobacteri
	13	247.8	18.6	13540	1	MTCI61	Z98260 Mycobacteri
	14	247.8	18.6	14629	1	AE007002	AE007002 Mycobacte
	15	247.8	18.6	75216	6	AX704275	AX704275 Sequence
	16	247.8	18.6	299450	1	BX248338	BX248338 Mycobacte
	17	236.2	17.8	348450	1	MLEPRTN4	AL583920 Mycobacte
	18	227.8	17.1	38675	1	MLU15180	U15180 Mycobacteri
c	19	205.4	15.4	320150	1	AP005033	AP005033 Streptomy
	20	203.8	15.3	311000	1	SCO939122	AL939122 Streptomy
	21	190	14.3	492	6	AX121326	AX121326 Sequence
	22	190	14.3	492	6	BD163443	BD163443 Novel pol
c	23	177	13.3	639	6	AX121324	AX121324 Sequence
c	24	177	13.3	639	6	BD163441	BD163441 Novel pol
c	25	72.8	5.5	92509	1	AL646086	AL646086 Ralstonia
	26	63.6	4.8	2900	1	AF144091	AF144091 Mycobacte
	27	58.4	4.4	308750	1	AP005216	AP005216 Corynebact
	28	58	4.4	2908	1	SAJ10320	AJ010320 Streptomy
	29	55.8	4.2	8046	1	AF049107	AF049107 Myxococcu
	30	53.8	4.0	651	6	AX023844	AX023844 Sequence
c	31	53.8	4.0	14683	1	AE007143	AE007143 Mycobacte
c	32	53.8	4.0	22070	1	MTCY7D11	Z95120 Mycobacteri
c	33	53.8	4.0	308050	1	BX248345	BX248345 Mycobacte

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1330	100.0	1330	10	US-09-935-757-1	instant	Sequence 1, Appli	
	2	1330	100.0	2086	10	US-09-935-757-5	"	Sequence 5, Appli	
	3	1330	100.0	3309400	10	US-09-738-626-1	Nakagawa	Sequence 1, Appli	
	4	639	48.0	639	10	US-09-738-626-1241		Sequence 1241, Ap	
	5	247.8	18.6	75216	15	US-10-080-170-646		Sequence 646, App	
	6	205.4	15.4	657	14	US-10-156-761-3104		Sequence 3104, Ap	
c	7	205.4	15.4	9025608	14	US-10-156-761-1		Sequence 1, Appli	
	8	190	14.3	492	10	US-09-738-626-1242		Sequence 1242, Ap	
c	9	177	13.3	639	10	US-09-738-626-1240		Sequence 1240, Ap	
	10	53.2	4.0	681	14	US-10-156-761-3025		Sequence 3025, Ap	
	11	52.6	4.0	618	10	US-09-738-626-855		Sequence 855, App	
	12	52.6	4.0	1148	10	US-09-942-936-1		Sequence 1, Appli	
	13	45.2	3.4	696	14	US-10-156-761-3872		Sequence 3872, Ap	
	14	45.2	3.4	9025608	14	US-10-156-761-1		Sequence 1, Appli	
	15	42.2	3.2	1211	10	US-09-942-935-1		Sequence 1, Appli	
	16	40.2	3.0	603	10	US-09-738-626-3416		Sequence 3416, Ap	
	17	39.2	2.9	2961	14	US-10-156-761-6965		Sequence 6965, Ap	
	18	37.4	2.8	591	14	US-10-156-761-6314		Sequence 6314, Ap	
	19	37.2	2.8	612	14	US-10-156-761-886		Sequence 886, App	
	20	37	2.8	618	14	US-10-156-761-6054		Sequence 6054, Ap	
	21	36.4	2.7	579	10	US-09-738-626-284		Sequence 284, App	
	22	36.4	2.7	1109	10	US-09-941-936A-1		Sequence 1, Appli	
c	23	36.4	2.7	3309400	10	US-09-738-626-1		Sequence 1, Appli	
	24	35.8	2.7	594	14	US-10-156-761-5107		Sequence 5107, Ap	
	25	35.6	2.7	261	14	US-10-156-761-3386		Sequence 3386, Ap	
	26	35.6	2.7	822	10	US-09-938-842A-2586		Sequence 2586, Ap	
	27	35.2	2.6	505	14	US-10-184-644-450		Sequence 450, App	
	28	35.2	2.6	505	14	US-10-184-634-450		Sequence 450, App	
	29	34.8	2.6	645	14	US-10-156-761-691		Sequence 691, App	
c	30	34.2	2.6	735	14	US-10-128-714-2495		Sequence 2495, Ap	
c	31	34.2	2.6	765	14	US-10-128-714-7495		Sequence 7495, Ap	
c	32	34.2	2.6	1076	14	US-10-128-714-1495		Sequence 1495, Ap	
c	33	34.2	2.6	1076	14	US-10-128-714-6495		Sequence 6495, Ap	
	34	34.2	2.6	2748	10	US-09-738-626-2853		Sequence 2853, Ap	
c	35	34.2	2.6	3076	14	US-10-128-714-495		Sequence 495, App	
c	36	34.2	2.6	3076	14	US-10-128-714-5495		Sequence 5495, Ap	
	37	33.8	2.5	1483	11	US-09-934-900-9		Sequence 9, Appli	
c	38	33.8	2.5	1827	8	US-08-976-063C-39		Sequence 39, Appl	
	39	33.8	2.5	3303	14	US-10-156-761-5384		Sequence 5384, Ap	
c	40	33.8	2.5	32679	8	US-08-976-063C-1		Sequence 1, Appli	
	41	33.8	2.5	88421	10	US-09-976-059-1		Sequence 1, Appli	
	42	33.6	2.5	498	10	US-09-974-300-1386		Sequence 1386, Ap	
c	43	33.4	2.5	10839	14	US-10-156-761-2882		Sequence 2882, Ap	
c	44	33.4	2.5	125746	14	US-10-156-761-15102		Sequence 15102, A	
c	45	33.2	2.5	612	13	US-10-027-632-269334		Sequence 269334,	

ALIGNMENTS

RESULT 1
US-09-935-757-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2003, 05:43:34 ; Search time 3526 Seconds
(without alignments)
9167.599 Million cell updates/sec

Title: US-09-935-757-1
Perfect score: 1330
Sequence: 1 accagtggagccgttgccat.....tcacctttcagcagacgccg 1330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	53.4	4.0	879	11	BC022210	BC022210 Homo sapi
	2	44.4	3.3	323	28	BH827253	BH827253 BACPP25-C
	3	44.4	3.3	542	28	BH823104	BH823104 BACPP18-H
c	4	44.4	3.3	626	10	BG458215	BG458215 NF052A09P
	5	44.4	3.3	626	28	BH832826	BH832826 BACPP4-G1
	6	42	3.2	968	29	BZ561490	BZ561490 pacs2-164
c	7	41.6	3.1	1201	13	BX376097	BX376097 BX376097
	8	41	3.1	1201	13	BX381961	BX381961 BX381961
	9	40.8	3.1	757	14	CB626552	CB626552 OSIIIEa16N
	10	40.8	3.1	1201	13	BX376097	BX376097 BX376097
	11	39.4	3.0	514	9	AI258010	AI258010 LP06566.5
	12	39.2	2.9	399	9	AJ517682	AJ517682 AJ517682
	13	39.2	2.9	672	14	CB655173	CB655173 OSJNEc08F
c	14	39.2	2.9	1201	9	AL540975	AL540975 AL540975
c	15	38.8	2.9	571	13	BQ542318	BQ542318 ps96f08.y
c	16	38.8	2.9	871	29	BZ675464	BZ675464 PUBEA48TD
c	17	38.6	2.9	546	10	BG438520	BG438520 ps27d06.y
	18	38.4	2.9	475	12	BM029212	BM029212 IpSkn0005
	19	38.4	2.9	645	29	BZ341454	BZ341454 ic45d12.g
	20	38.4	2.9	893	13	BQ931778	BQ931778 AGENCOURT
	21	38.2	2.9	664	29	BZ405741	BZ405741 OGACG81TM
c	22	38	2.9	252	9	AV321071	AV321071 AV321071
c	23	38	2.9	474	13	BQ768312	BQ768312 EBro08_SQ
	24	38	2.9	854	29	CNS013C9	AL102675 Drosophil
c	25	37.8	2.8	334	14	CA550740	CA550740 C0834E08-
c	26	37.8	2.8	483	14	CA548840	CA548840 C0810G09-
	27	37.8	2.8	1201	13	BX461310	BX461310 BX461310
	28	37.6	2.8	721	10	BG565144	BG565144 602583771
	29	37.6	2.8	1100	10	AW982688	AW982688 HVSMEg000
	30	37.4	2.8	590	28	BH801677	BH801677 1008119C0
	31	37.2	2.8	625	28	AZ409252	AZ409252 1M0180B07
c	32	37.2	2.8	665	14	CD430773	CD430773 ETH1_5_E1
	33	37.2	2.8	885	13	BX425603	BX425603 BX425603
c	34	37	2.8	309	10	BF044168	BF044168 BP250012B
	35	37	2.8	555	13	BQ237637	BQ237637 TaE05014C
	36	36.8	2.8	747	29	BZ984887	BZ984887 PUGGT51TB
c	37	36.4	2.7	435	10	BE423917	BE423917 WHE0067_A
c	38	36.4	2.7	657	13	BQ410640	BQ410640 GA_Ed003
	39	36.4	2.7	852	13	BX393687	BX393687 BX393687
	40	36.4	2.7	1101	29	CNS00AWK	AL056026 Drosophil
c	41	36.2	2.7	496	13	BY490020	BY490020 BY490020
c	42	36.2	2.7	713	28	AQ577720	AQ577720 nbxb0091F
c	43	36.2	2.7	852	29	BZ567068	BZ567068 pacs2-164
c	44	36.2	2.7	997	29	CNS006DN	AL065132 Drosophil
	45	36.2	2.7	1063	29	BZ561504	BZ561504 pacs2-164